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RAW SEQUENCE LISTING PATENT APPLICATION US/10/067,477

DATE: 05/02/2002 TIME: 15:07:19

INPUT SET: \$36844.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

```
SEQUENCE LISTING
        3
           (1)
                  General Information:
                (1) GENERAL INFORMATION:
                (i) APPLICANT:
            (A) NAME: Shuji HINUMA
-->
            (B) STREET: 7-9-1402, Kasuga 1-chome
                                                                ENTERED
             (C) CITY: Tsukuba
-->
        9
            (D) STATE: Ibaraki
       10
           (E) COUNTRY: Japan
       11
            (F) POSTAL CODE (ZIP): 305
       12
          APPLICANT:
       13
             (A) NAME: Junichi SAKAMOTO
       14
       15
             (B) STREET: 14-30-A103, Kamishinden 1-chome
       16
             (C) CITY: Toyonaka
       17
             (D) STATE: Osaka
       18
             (E) COUNTRY: Japan
      19
             (F) POSTAL CODE (ZIP): 565
       20
           APPLICANT:
       21
       22
             (A) NAME: Masaki HOSOYA
       23
             (B) STREET: 711-83, Itaya 1-chome
       24
             (C) CITY: Tsuchiura
       25
             (D) STATE: Ibaraki
       26
             (E) COUNTRY: Japan
       27
             (F) POSTAL CODE (ZIP): 300
       28
       29
               (ii) TITLE OF INVENTION: G Protein Coupled Receptor Proteins,
       30
            Their Production And Use
       31
      32
              (iii) NUMBER OF SEQUENCES: 19
      33
      34
               (iv) CORRESPONDENCE ADDRESS:
      35
             (A) ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
      36
             (B) STREET: 130 Water Street
      37
             (C) CITY: Boston
      38
             (D) STATE: MA
      39
             (E) COUNTRY: USA
      40
             (F) ZIP: 02109
      41
      42
                (v) COMPUTER READABLE FORM:
      43
             (A) MEDIUM TYPE: Diskette
      44
             (B) COMPUTER: IBM Compatible
      45
             (C) OPERATING SYSTEM: DOS
             (D) SOFTWARE: FastSEQ Version 1.5
      46
```

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47
       (vi) CURRENT APPLICATION DATA:
48
      (A) APPLICATION NUMBER: 10/067,477
49
      (B) FILING DATE:
50
51
      (C) CLASSIFICATION
52
       (vii) PRIOR APPLICATION DATA:
53
54
55
            (A) APPLICATION NUMBER: 08/796,570
56
      (B) FILING DATE: 06-FEB-1997
57
58
59
      (A) APPLICATION NUMBER: Japan 8-021562
      (B) FILING DATE: 2-JUL-1996
60
61
       (viii) ATTORNEY/AGENT INFORMATION:
62
63
      (A) NAME: Eisenstein, Ronald I.
      (B) REGISTRATION NUMBER: 30.628
64
      (C) REFERENCE/DOCKET NUMBER: 47147
65
66
67
         (ix) TELECOMMUNICATION INFORMATION:
68
      (A) TELEPHONE: 617-523-3400
      (B) TELEFAX: 617-523-6440
69
70
   (2) INFORMATION FOR SEQ ID NO:1:
71
         (i) SEQUENCE CHARACTERISTICS:
72
      (A) LENGTH: 423
73
74
      (B) TYPE:
                    Amino acid
      (C) TOPOLOGY: Linear
75
        (ii) MOLECULE TYPE: Peptide
76
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
77
78
    Met Val Pro His Leu Leu Leu Cys Leu Leu Pro Leu Val Arg Ala
79
80
                   5
                                         10
    Thr Glu Pro His Glu Gly Arg Ala Asp Glu Gln Ser Ala Glu Ala Ala
81
                                                 30
82
       20
                             25
83
    Leu Ala Val Pro Asn Ala Ser His Phe Phe Ser Trp Asn Asn Tyr Thr
                        40
                                            45
84
85
    phe Ser Asp Trp Gln Asn Phe Val Gly Arg Arg Arg Tyr Gly Ala Glu
86
    Ser Gln Asn Pro Thr Val Lys Ala Leu Leu Ile Val Ala Tyr Ser Phe
87
88
                         70
                                             75
    Ile Ile Val Phe Ser Leu Phe Gly Asn Val Leu Val Cys His Val Ile
89
                                             95
90
                         90
    Phe Lys Asn Gln Arg Met His Ser Ala Thr Ser Leu Phe Ile Val Asn
91
                                               110
92
      100
                           105
    Leu Ala Val Ala Asp Ile Met Ile Thr Leu Leu Asn Thr Pro Phe Thr
93
94
                        120
                                            125
    Leu Val Arg Phe Val Asn Ser Thr Trp Ile Phe Gly Lys Gly Met Cys
95
96
      130
                          135
                                             140
    His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu His Val Ser Ala Leu
97
98
    145
                        150
                                            155
   Thr Leu Thr Ala Ile Ala Val Asp Arg His Gln Val Ile Met His Pro
99
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170
                                             175
100
101
     Leu Lys Pro Arg Ile Ser Ile Thr Lys Gly Val Ile Tyr Ile Ala Val
102
        180
                             185
                                                 190
     Ile Trp Thr Met Ala Thr Phe Phe Ser Leu Pro His Ala Ile Cvs Gln
103
104
                         200
                                             205
     Lys Leu Phe Thr Phe Lys Tyr Ser Glu Asp Ile Val Arg Ser Leu Cys
105
106
                             215
107
     Leu Pro Asp Phe Pro Glu Pro Ala Asp Leu Phe Trp Lys Tyr Leu Asp
108
                         230
                                             235
109
     Leu Ala Thr Phe Ile Leu Leu Tyr Ile Leu Pro Leu Leu Ile Ile Ser
110
                         250
                                             255
     Val Ala Tyr Ala Arg Val Ala Lys Lys Leu Trp Leu Cys Asn Met Ile
111
112
                            265
     Gly Asp Val Thr Thr Glu Gln Tvr Phe Ala Leu Arg Arg Lys Lys Lys
113
114
                         280
                                             285
     Lys Thr Ile Lys Met Leu Met Leu Val Val Leu Phe Ala Leu Cys
115
116
         290
                                                300
                             295
117
     Trp Phe Pro Leu Asn Cys Tyr Val Leu Leu Ser Ser Lys Val Ile
118
                         310
                                            315
119
     Arg Thr Asn Asn Ala Leu Tyr Phe Ala Phe His Trp Phe Ala Met Ser
120
                         330
                                             335
121
     Ser Thr Cys Tyr Asn Pro Phe Ile Tyr Cys Trp Leu Asn Glu Asn Phe
122
                             345
                                                350
123
     Arg Ile Glu Leu Lys Ala Leu Leu Ser Met Cys Gln Arg Pro Pro Lys
124
                         360
                                             365
125
     Pro Gln Glu Asp Arg Pro Pro Ser Pro Val Pro Ser Phe Arg Val Ala
126
      370
                             375
127
     Trp Thr Glu Lys Asn Asp Gly Gln Arg Ala Pro Leu Ala Asn Asn Leu
128
                         390
                                            395
                                                               400
129
     Leu Pro Thr Ser Gln Leu Gln Ser Gly Lys Thr Asp Leu Ser Ser Val
130
                         410
131
     Glu Pro Ile Val Thr Met Ser
132
        420
133
     (2) INFORMATION FOR SEO ID NO:2:
134
135
          (i) SEQUENCE CHARACTERISTICS:
136
       (A) LENGTH:
                   1272
137
       (B) TYPE:
                     Nucleic acid
138
       (C) STRANDEDNESS: Double
139
       (C) TOPOLOGY: Linear
140
         (ii) MOLECULE TYPE: cDNA
141
         (xi) FEATURE:
142
       (C) IDENTIFICATION METHOD: S
143
          (xi) SEOUENCE DESCRIPTION: SEO ID NO:2:
144
145
     ATGGTCCCTC ACCTCTTGCT GCTCTGTCTC CTCCCCTTGG TGCGAGCCAC CGAGCCCCAC
146
    GAGGGCCGGG CCGACGAGCA GAGCGCGGAG GCGGCCCTGG CCGTGCCCAA TGCCTCGCAC 120
147
     TTCTTCTCTT GGAACAACTA CACCTTCTCC GACTGGCAGA ACTTTGTGGG CAGGAGGCGC
148
     TACGGCGCTG AGTCCCAGAA CCCCACGGTG AAAGCCCTGC TCATTGTGGC TTACTCCTTC
                                                                       240
149
     ATCATTGTCT TCTCACTCTT TGGCAACGTC CTGGTCTGTC ATGTCATCTT CAAGAACCAG
                                                                       300
150 CGAATGCACT CGGCCACCAG CCTCTTCATC GTCAACCTGG CAGTTGCCGA CATAATGATC
                                                                       360
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151 ACGCTGCTCA ACACCCCCTT CACTTTGGTT CGCTTTGTGA ACAGCACATG GATATTTGGG 420
152 AAGGGCATGT GCCATGTCAG CCGCTTTGCC CAGTACTGCT CACTGCACGT CTCAGCACTG 480

205

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153 ACACTGACAG CCATTGCGGT GGATCGCCAC CAGGTCATCA TGCACCCCTT GAAACCCCGG 540
     ATCTCAATCA CAAAGGGTGT CATCTACATC GCTGTCATCT GGACCATGGC TACGTTCTTT 600
154
155
     TCACTCCCAC ATGCTATCTG CCAGAAATTA TTTACCTTCA AATACAGTGA GGACATTGTG 660
156 CGCTCCCTCT GCCTGCCAGA CTTCCCTGAG CCAGCTGACC TCTTCTGGAA GTACCTGGAC 720
157 TTGGCCACCT TCATCCTGCT CTACATCCTG CCCCTCCTCA TCATCTCTGT GGCCTACGCT 780
158 CGTGTGGCCA AGAAACTGTG GCTGTGTAAT ATGATTGGCG ATGTGACCAC AGAGCAGTAC 840
159 TTTGCCCTGC GGCGCAAAAA GAAGAAGACC ATCAAGATGT TGATGCTGGT GGTAGTCCTC 900
160 TTTGCCCTCT GCTGGTTCCC CCTCAACTGC TACGTCCTCC TCCTGTCCAG CAAGGTCATC 960
161 CGCACCAACA ATGCCCTCTA CTTTGCCTTC CACTGGTTTG CCATGAGCAG CACCTGCTAT 1020
162 AACCCCTTCA TATACTGCTG GCTGAACGAG AACTTCAGGA TTGAGCTAAA GGCATTACTG 1080
1.63
    AGCATGTGTC AAAGACCTCC CAAGCCTCAG GAGGACAGGC CACCCTCCCC AGTTCCTTCC 1140
    TTCAGGGTGG CCTGGACAGA GAAGAATGAT GGCCAGAGGG CTCCCCTTGC CAATAACCTC 1200
164
    CTGCCCACCT CCCAACTCCA GTCTGGGAAG ACAGACCTGT CATCTGTGGA ACCCATTGTG 1260
165
166
    ACGATGAGTT AG
167
    (2) INFORMATION FOR SEQ ID NO:3:
168
      (i) SEQUENCE CHARACTERISTICS:
169
170
       (A) LENGTH: 70
171
       (B) TYPE:
                    Amino acid
172
       (C) TOPOLOGY: Linear
173
        (ii) MOLECULE TYPE: Peptide
174
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
175
176
    Val Cys His Val Ile Phe Lys Asn Gln Arg Met His Ser Ala Thr Ser
177
     1
                                        10
178
    Leu Phe Ile Val Asn Leu Ala Val Ala Asp Ile Met Ile Thr Leu Leu
179
      20
                            25
                                               30
180
     Asn Thr Pro Phe Thr Leu Val Arg Phe Val Asn Ser Thr Trp Ile Phe
181
    35
                   40
                                        4.5
     Gly Lys Gly Met Cys His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu
182
183
       50
184
     His Val Ser Ala Leu Thr
185
     65
186
    (2) INFORMATION FOR SEO ID NO:4:
187
188
         (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 71
189
190
       (B) TYPE:
                     Amino acid
       (C) TOPOLOGY: Linear
191
        (ii) MOLECULE TYPE: Peptide
192
193
         (xi) SEQUENCE DESCRIPTION: SEO ID NO:4:
194
    Glu Pro Ala Asp Leu Phe Trp Lys Asn Leu Asp Leu Pro Thr Phe Ile
195
196
                   5 10
    Leu Leu Asn Ile Leu Pro Leu Leu Ile Ile Ser Val Ala Tyr Val Arg
197
      20
198
                    25
                                              3.0
199
    Val Thr Lys Lys Leu Trp Leu Cys Asn Met Ile Val Asp Val Thr Thr
200
                        40
                                           45
     Glu Gln Tyr Phe Ala Leu Arg Pro Lys Lys Lys Thr Ile Lys Met
201
202
     50
                         55
                                               60
     Leu Met Leu Val Val Val Leu
203
204
     65
                        70
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206
    (2) INFORMATION FOR SEQ ID NO:5:
207
          (i) SEQUENCE CHARACTERISTICS:
208
        (A) LENGTH:
                      210
209
       (B) TYPE:
                      Nucleic acid
       (C) STRANDEDNESS:
210
                           Double
       (C) TOPOLOGY: Linear
211
         (ii) MOLECULE TYPE: cDNA
212
213
         (xi) FEATURE:
214
       (C) IDENTIFICATION METHOD: S
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
215
216
217 GTCTGTCATG TCATCTTCAA GAACCAGCGA ATGCACTCGG CCACCAGCCT CTTCATCGTĆ
                                                                        60
218 AACCTGGCAG TTGCCGACAT AATGATCACG CTGCTCAACA CCCCCTTCAC TTTGGTTCGC 120
219 TTTGTGAACA GCACATGGAT ATTTGGGAAG GGCATGTGCC ATGTCAGCCG CTTTGCCCAG 180
220 TACTGCTCAC TGCACGTCTC AGCACTGACA
                                                                       210
221
222
     (2) INFORMATION FOR SEO ID NO:6:
223
          (i) SEOUENCE CHARACTERISTICS:
        (A) LENGTH: 213
224
225
       (B) TYPE:
                     Nucleic acid
226
       (C) STRANDEDNESS: Double
227
       (C) TOPOLOGY: Linear
228
        (ii) MOLECULE TYPE: cDNA
229
         (xi) FEATURE:
230
       (C) IDENTIFICATION METHOD: S
231
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
232
233 GAGCCAGCTG ACCTCTTCTG GAAGAACCTG GACTTGCCCA CCTTCATCCT GCTCAACATC
234 CTGCCCCTCC TCATCATCTC TGTGGCCTAC GTTCGTGTGA CCAAGAAACT GTGGCTGTGT 120
235 AATATGATTG TCGATGTGAC CACAGAGCAG TACTTTGCCC TGCGGCCCAA AAAGAAGAAG 180
236 ACCATCAAGA TGTTGATGCT GGTGGTAGTC CTC
                                                                       213
237
238 (2) INFORMATION FOR SEQ ID NO:7:
          (i) SEQUENCE CHARACTERISTICS:
239
240
       (A) LENGTH:
                           25
       (B) TYPE:
241
                           Nucleic acid
242
       (C) STRANDEDNESS:
                         Single
       (C) TOPOLOGY:
243
                          Linear
244
        (ii) MOLECULE TYPE: Other nucleic acid Synthetic
           DNA
245
         (xi) SEOUENCE DESCRIPTION: SEO ID NO:7:
246
247
248 CGTGGSCMTS STGGGCAACN YCCTG
                                      25
249
250 (2) INFORMATION FOR SEO ID NO:8:
          (i) SEQUENCE CHARACTERISTICS:
251
252
       (A) LENGTH:
                          27
253
       (B) TYPE:
                           Nucleic acid
       (C) STRANDEDNESS:
254
                         Single
255
       (C) TOPOLOGY:
                         Linear
        (ii) MOLECULE TYPE:
                                Other nucleic acid Synthetic
256
257
          DNA
         (xi) SEQUENCE DESCRIPTION: SEO ID NO:8:
258
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SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/10/067,477

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Line	Error	Original Text
5 6 7 8 9 10 11 14 15 16 17 18	Mandatory Value Not Present Unknown or Misplaced Identifier	(i) APPLICANT: (A) NAME: Shuji HINUMA (B) STREET: 7-9-1402, Kasuga 1-chome (C) CITY: Tsukuba (D) STATE: Ibaraki (E) COUNTRY: Japan (F) POSTAL CODE (ZIP): 305 (A) NAME: Junichi SAKAMOTO (B) STREET: 14-30-A103, Kamishinden 1-chome (C) CITY: Toyonaka (D) STATE: Osaka (E) COUNTRY: Japan (F) POSTAL CODE (ZIP): 565
22 23 24	Unknown or Misplaced Identifier Unknown or Misplaced Identifier Unknown or Misplaced Identifier	(A) NAME: Masaki HOSOYA (B) STREET: 711-83, Itaya 1-chome (C) CITY: Tsuchiura
18 19 22	Unknown or Misplaced Identifier Unknown or Misplaced Identifier Unknown or Misplaced Identifier	(E) COUNTRY: Japan (F) POSTAL CODE (ZIP): 565 (A) NAME: Masaki HOSOYA
25 26 27	Unknown or Misplaced Identifier Unknown or Misplaced Identifier Unknown or Misplaced Identifier	(D) STATE: Ibaraki (E) COUNTRY: Japan (F) POSTAL CODE (ZIP): 300

PAGE: 1

SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/10/067,477

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GENERAL INFORMATION More Identifiers Found Than MAX Allowed

PAGE: 1

SEQUENCE CORRECTION REPORT PATENT APPLICATION US/10/067,477

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Line	Original Text	Corrected Text
51 138 141 210 213 226 229	(C) CLASSIFICATION (C) STRANDENESS: Double (xi) FEATURE (C) STRANDENESS: Double (xi) FEATURE (C) STRANDENESS: Double (xi) FEATURE	(C) CLASSIFICATION: (C) STRANDEDNESS: Double (xi) FEATURE: (C) STRANDEDNESS: Double (xi) FEATURE: (C) STRANDEDNESS: Double (xi) FEATURE: